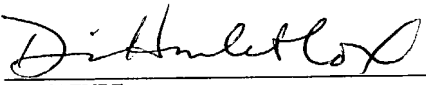


09720530.031202

414 Rec'd PCT/PTO 19 DEC 2000 PCT

FORM PTO-1390 U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371		ATTORNEY'S DOCKET NUMBER PF-0551 USN
		U.S. APPLICATION NO. (If known, see 37 CFR 1.55 TO BE ASSIGNED) 09/720530
INTERNATIONAL APPLICATION NO. PCT/US99/15121	INTERNATIONAL FILING DATE 2 July 1999	PRIORITY DATE CLAIMED 2 July 1998
TITLE OF INVENTION NEUROTRANSMISSION ASSOCIATED PROTEINS		
APPLICANT(S) FOR DO/EO/US INCYTE PHARMACEUTICALS, INC.; LAL, Preeti; TANG, Y. Tom; YUE, Henry; CORLEY, Neil C.; GUEGLER, Karl J.; GORGONE, Gina A.; BAUGHN, Mariah R.; PATTERSON, Chandra		
<p>Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:</p> <ol style="list-style-type: none"><input checked="" type="checkbox"/> This is the FIRST submission of items concerning a filing under 35 U.S.C. 371.<input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.<input type="checkbox"/> This is an express request to promptly begin national examination procedures (35 U.S.C. 371 (f)).<input type="checkbox"/> The US has been elected by the expiration of 19 months from the priority date (PCT Article 31).<input checked="" type="checkbox"/> A copy of the International Application as filed (35 U.S.C. 371(c)(2))<ol style="list-style-type: none"><input type="checkbox"/> is attached hereto (required only if not communicated by the International Bureau)<input type="checkbox"/> has been communicated by the International Bureau.<input checked="" type="checkbox"/> is not required, as the application was filed in the United States Receiving Office (RO/US).<input type="checkbox"/> An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)).<input checked="" type="checkbox"/> Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))<ol style="list-style-type: none"><input type="checkbox"/> are attached hereto (required only if not communicated by the International Bureau).<input type="checkbox"/> have been communicated by the International Bureau.<input type="checkbox"/> have not been made; however, the time limit for making such amendments has NOT expired.<input checked="" type="checkbox"/> have not been made and will not be made.<input type="checkbox"/> An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).<input type="checkbox"/> An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).<input type="checkbox"/> An English language translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).		
Items 11 to 16 below concern document(s) or information included:		
<ol style="list-style-type: none"><input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98.<input type="checkbox"/> An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.27 and 3.31 is included.<input type="checkbox"/> A FIRST preliminary amendment. <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment.<input type="checkbox"/> A substitute specification.<input type="checkbox"/> A change of power of attorney and/or address letter.<input checked="" type="checkbox"/> Other items or information: 1) Transmittal Letter (2 pp, in duplicate) 2) Return Postcard 3) Express Mail Label No.: EL 743 380 000 US		

U.S. APPLICATION NO. (if known, see 37 CFR 1.5) TO BE ASSIGNED: 09/720530		INTERNATIONAL APPLICATION NO.: PCT/US99/15121		ATTORNEY'S DOCKET NUMBER PF-0551 USN	
17. <input type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)): Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO..... \$1000.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO.. \$860.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO..... \$710.00 <input checked="" type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) but all claims did not satisfy provisions of PCT Article 33(1)-(4)..... \$690.00 International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4)..... \$100.00					
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$690.00	
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)).				\$	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total Claims	21 =	1	X \$ 18.00	\$ 18.00	
Independent Claims	2 =	0	X \$ 80.00	\$	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$270.00	\$	
TOTAL OF ABOVE CALCULATIONS =				\$708.00	
<input type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27. The fees indicated above are reduced by 1/2.				\$	
SUBTOTAL =				\$708.00	
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).				\$	
TOTAL NATIONAL FEE =				\$708.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by the appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property +				\$	
TOTAL FEES ENCLOSED =				\$708.00	
				Amount to be Refunded:	\$
				Charged:	\$
a. <input type="checkbox"/> A check in the amount of \$ _____ to cover the above fees is enclosed. b. <input checked="" type="checkbox"/> Please charge my Deposit Account No. <u>09-0108</u> in the amount of \$ <u>708.00</u> to cover the above fees. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>09-0108</u> . A duplicate copy of this sheet is enclosed.					
NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.					
SEND ALL CORRESPONDENCE TO: INCYTE GENOMICS, INC. 3160 Porter Drive Palo Alto, CA 94304					
 SIGNATURE					
NAME: Diana Hamlet-Cox					
REGISTRATION NUMBER: 33,302					
DATE: <u>19</u> December 2000					

PTO/PCT Rec'd 19 DEC 2000

NEUROTRANSMISSION ASSOCIATED PROTEINS**TECHNICAL FIELD**

5 This invention relates to nucleic acid and amino acid sequences of neurotransmission associated proteins and to the use of these sequences in the diagnosis, treatment, and prevention of cancer and immune and neurological disorders.

BACKGROUND OF THE INVENTION

10 Neurotransmission is the basic process of transmitting nerve signals, in the form of electrical and chemical impulses, between nerve cells which carry signals from sensory receptors (e.g., for light, touch, pressure, odor and taste) to the brain, and similar signals from the brain to effector targets or organs such as skeletal or smooth muscle. The nervous system is composed of the central nervous system (CNS), consisting of the brain and spinal cord, and the peripheral
15 nervous system (PNS), consisting of afferent neural pathways for conducting nerve impulses from sensory organs to the CNS, and efferent neural pathways for conducting motor impulses from the CNS to effector organs. The PNS can be further divided into the somatic nervous system, which regulates voluntary motor activity such as for skeletal muscle, and the autonomic nervous system, which regulates involuntary motor activity for internal organs such as the heart, lungs, and viscera.

20 The basic cellular unit of neurotransmission is the nerve cell, or neuron. The process of neurotransmission involves the transmission of a neural signal between neurons by means of a combination of electrical and chemical impulses. The process begins with the stimulation of a nerve and the generation of an electrical impulse at which travels along the axon of the neuron to its terminus. Neurons are separated from one another by a space (the synapse or synaptic cleft)
25 which must be bridged to transmit the signal to another neuron. This accomplished by a specialized form of vesicle transport which uses a neurotransmitter signaling molecule stored in a membrane-bound synaptic vesicle at the terminus of the neuron. A change in electrical potential at the nerve terminal resulting from the electrical impulse triggers the release of the neurotransmitter from the synaptic vesicle by exocytosis. The neurotransmitter rapidly diffuses
30 across the synaptic cleft separating the presynaptic nerve cell from the postsynaptic cell and provokes a change in electrical potential in the latter by binding to receptors and opening transmitter-gated ion channels located in the plasma membrane of the postsynaptic cell. The change in membrane potential of the postsynaptic cell may serve either to excite or inhibit further transmission of the nerve impulse.

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Neurotransmitters comprise a diverse group of some 30 substances which include acetylcholine, monoamines such as serotonin, dopamine, and histamine, and amino acids such as gamma-aminobutyric acid (GABA), glutamate, and aspartate, and neuropeptides such as endorphins and enkephalins. (McCance, K.L. and Huether, S.E. (1994) PATHOPHYSIOLOGY,

5 The Biologic Basis for Disease in Adults and Children, 2nd edition, Mosby, St. Louis, MO, pp 403-404.) Many of these molecules have more than one function and the effects may be excitatory, e.g. to depolarize the postsynaptic cell plasma membrane and stimulate nerve impulse transmission, or inhibitory, e.g. to hyperpolarize the plasma membrane and inhibit nerve impulse transmission.

10 Neurotransmitters and their receptors are targets of pharmacological agents aimed at controlling neurological function. For example GABA is the major inhibitory neurotransmitter in the CNS, and GABA receptors are the principal target of sedatives such as benzodiazepines and barbiturates which act by enhancing GABA mediated effects. (Katzung, B.G. (1995) Basic and Clinical Pharmacology, 6th edition, Appleton & Lange, Norwalk, CT, pp. 338-339) Aberrant
15 activity of neurotransmitters and their receptors are involved in various neurological conditions. Alzheimer's disease is associated with a decrease in acetylcholine-secreting neurons, and myasthenia gravis results from a reduction in acetylcholine receptors. Destruction of dopamine-secreting receptors and overstimulation of N-methyl-D-aspartate (NMDA) receptors in the brain is implicated in neuronal cell death associated with disorders such as stroke, epilepsy, Parkinson's
20 disease and Alzheimer's disease. (Planells-Cases, R. Et al. (1993) Proc. Natl. Acad. Sci. USA 90:5057-5061.)

Various molecules are associated with synaptic vesicles that store and transport neurotransmitters. Synaptic vesicles of mature neurons have been shown to possess a specific complement of membrane proteins which are restricted to these vesicles, and at least 15 synaptic
25 vesicle proteins have been characterized. (Sudhof, T.C. and Jahn, R. (1991) Neuron 6:665-677.) Synaptophysin and synaptogyrin are two such proteins that colocalize in synaptic vesicle preparations. (Stenius, K. et al. (1995) J. Cell Biology 131:1801-1809.) The precise functions of these proteins in neurosecretion are unknown. Both have four transmembrane domains and are highly expressed in neuronal tissues, but may have nonneuronal isoforms as well. Syntaxins are
30 another family of proteins which are involved in synaptic vesicle transport, are associated with the plasma membrane of the neuron, and function as recognition sites for docking of the synaptic vesicle with the plasma membrane. Syntaxin interacts with complementary proteins on the synaptic vesicle (v-SNARES) to form a complex that initiates fusion of the vesicle with the plasma membrane prior to release of the neurotransmitter into the synapse. (Bock, J.B. et al. (1996) J.
35 Biol. Chem. 271:17961-17965.)

Various proteins are also associated with the sensory response to stimuli in organs that trigger a nerve signal. Rhodopsin is the photosensitive protein in rod cells of the eye that undergoes a conformational change during the absorption of light by an associated chromophore, retinal. This conformational change initiates a photochemical cascade that leads to a nerve signal.

- 5 Odorant detection is mediated by receptor neurons in the olfactory mucosa and also involves distinct odorant-binding proteins that act to bind and carry specific odorant molecules across the mucus layer to odorant receptor sites. (Dear, T.N. et al. (1991) EMBO Journal 10:2813-2819.)

- The discovery of new neurotransmission associated proteins and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the
10 diagnosis, treatment, and prevention of cancer and immune and neurological disorders.

SUMMARY OF THE INVENTION

- The invention features substantially purified polypeptides, neurotransmission associated proteins referred to collectively as "NTAP". In one aspect, the invention provides a substantially
15 purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6 (SEQ ID NO:1-6), and fragments thereof.

- The invention further provides a substantially purified variant having at least 90% amino acid identity to the amino acid sequences of SEQ ID NO:1-6, or to a fragment of any of these
20 sequences. The invention also provides an isolated and purified polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-6, and fragments thereof. The invention also includes an isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting
25 of SEQ ID NO:1-6, and fragments thereof.

- Additionally, the invention provides an isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-6, and fragments thereof, as well as an isolated and purified polynucleotide having a sequence which is
30 complementary to the polynucleotide encoding the polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:1-6, and fragments thereof.

The invention also provides an isolated and purified polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:12 (SEQ ID NO:7-12), and fragments

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thereof. The invention further provides an isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide sequence comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:7-12, and fragments thereof, as well as an isolated and purified polynucleotide having a sequence which is

5 complementary to the polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:7-12, and fragments thereof.

The invention further provides an expression vector containing at least a fragment of the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-6, and fragments thereof. In another aspect, the expression

10 vector is contained within a host cell.

The invention also provides a method for producing a polypeptide, the method comprising the steps of: (a) culturing the host cell containing an expression vector containing at least a fragment of a polynucleotide encoding the polypeptide under conditions suitable for the expression of the polypeptide; and (b) recovering the polypeptide from the host cell culture.

15 The invention also provides a pharmaceutical composition comprising a substantially purified polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:1-6, and fragments thereof in conjunction with a suitable pharmaceutical carrier.

The invention further includes a purified antibody which binds to a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:1-6, and

20 fragments thereof, as well as a purified agonist and a purified antagonist to the polypeptide.

The invention also provides a method for treating or preventing a cancer, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-6, and fragments thereof.

25 The invention also provides a method for treating or preventing an immune disorder, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-6, and fragments thereof.

The invention also provides a method for treating or preventing a neurological disorder,

30 the method comprising administering to a subject in need of such treatment an effective amount of a pharmaceutical composition comprising a substantially purified polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-6, and fragments thereof.

The invention also provides a method for detecting a polynucleotide, the method comprising the steps of: (a) hybridizing the complement of the polynucleotide sequence encoding

35 the polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID

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NO: 1-6, and fragments thereof to at least one of the nucleic acids of the biological sample, thereby forming a hybridization complex; and (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of a polynucleotide in the biological sample. In one aspect, the method further comprises amplifying the polynucleotide
 5 prior to hybridization.

BRIEF DESCRIPTION OF THE TABLES

In Table 1, columns 1 and 2 show the sequence identification numbers (SEQ ID NO:) of the amino acid and nucleic acid sequence, respectively. Column 3 shows the Clone ID of the
 10 Incyte Clone in which nucleic acids encoding each NTAP were first identified, and column 4, the cDNA library of this clone. Column 5 is entitled fragments, and shows the Incyte clones (and libraries) and shotgun sequences useful as fragments in hybridization technologies, and which are part of the consensus nucleotide sequence of each NTAP.

The columns of table 2 show various properties of the polypeptides of the invention:
 15 column 1 references the SEQ ID NO; column 2 shows the number of amino acid residues; column 3, potential phosphorylation sites; column 4, potential glycosylation sites; column 5, signature sequences associated with known proteins; column 6, the identity of the protein; and column 7, analytical methods used to identify the protein through sequence homologies and protein motifs.

The columns of table 3 show the tissue expression of each nucleic acid sequence by
 20 northern analysis, diseases or disorders associated with this tissue expression, and the vector into which each cDNA was cloned.

Table 4 shows the SEQ ID NO:, Incyte clone number and the associated library in which nucleic acid sequences encoding NTAP were first identified, and a brief description of the library.

Table 5 shows the programs/algorithms, descriptions, references and threshold parameters
 25 used to identify and characterize NTAP.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular methodology, protocols, cell lines, vectors, and reagents described, as these may vary. It is also to be understood that the terminology
 30 used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an

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antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods, devices, and materials are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

"NTAP," as used herein, refers to the amino acid sequences, or variant thereof, of substantially purified NTAP obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and preferably the human species, from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term "agonist," as used herein, refers to a molecule which, when bound to NTAP, increases or prolongs the duration of the effect of NTAP. Agonists may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to and modulate the effect of NTAP.

An "allelic variant," as this term is used herein, is an alternative form of the gene encoding NTAP. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. Any given natural or recombinant gene may have none, one, or many allelic forms. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding NTAP, as described herein, include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polynucleotide the same as NTAP or a polypeptide with at least one functional characteristic of NTAP. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding NTAP, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding NTAP. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues

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which produce a silent change and result in a functionally equivalent NTAP. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of NTAP is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, positively charged amino acids may include lysine and arginine, and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine, and valine; glycine and alanine; asparagine and glutamine; serine and threonine; and phenylalanine and tyrosine.

The terms "amino acid" or "amino acid sequence," as used herein, refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. In this context, "fragments," "immunogenic fragments," or "antigenic fragments" refer to fragments of NTAP which are preferably at least 5 to about 15 amino acids in length, most preferably at least 14 amino acids, and which retain some biological activity or immunological activity of NTAP. Where "amino acid sequence" is recited herein to refer to an amino acid sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification," as used herein, relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art. (See, e.g., Dieffenbach, C.W. and G.S. Dveksler (1995) PCR Primer, a Laboratory Manual, Cold Spring Harbor Press, Plainview, NY, pp.1-5.)

The term "antagonist," as it is used herein, refers to a molecule which, when bound to NTAP, decreases the amount or the duration of the effect of the biological or immunological activity of NTAP. Antagonists may include proteins, nucleic acids, carbohydrates, antibodies, or any other molecules which decrease the effect of NTAP.

As used herein, the term "antibody" refers to intact molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind NTAP polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant," as used herein, refers to that fragment of a molecule

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(i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (given regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense," as used herein, refers to any composition containing a nucleic acid sequence which is complementary to the "sense" strand of a specific nucleic acid sequence. Antisense molecules may be produced by any method including synthesis or transcription. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form duplexes and to block either transcription or translation. The designation "negative" can refer to the antisense strand, and the designation "positive" can refer to the sense strand.

As used herein, the term "biologically active," refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" refers to the capability of the natural, recombinant, or synthetic NTAP, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The terms "complementary" or "complementarity," as used herein, refer to the natural binding of polynucleotides by base pairing. For example, the sequence "5' A-G-T 3'" binds to the complementary sequence "3' T-C-A 5'." Complementarity between two single-stranded molecules may be "partial," such that only some of the nucleic acids bind, or it may be "complete," such that total complementarity exists between the single stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands. This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands, and in the design and use of peptide nucleic acid (PNA) molecules.

A "composition comprising a given polynucleotide sequence" or a "composition comprising a given amino acid sequence," as these terms are used herein, refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding NTAP or fragments of NTAP may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts, e.g., NaCl, detergents, e.g., sodium dodecyl sulfate (SDS), and other components, e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.

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“Consensus sequence,” as used herein, refers to a nucleic acid sequence which has been resequenced to resolve uncalled bases, extended using XL-PCR™ kit (Perkin-Elmer, Norwalk, CT) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from the overlapping sequences of more than one Incyte Clone using a computer program for fragment assembly, such as the GELVIEW™ Fragment Assembly system (GCG, Madison, WI). Some sequences have been both extended and assembled to produce the consensus sequence.

As used herein, the term “correlates with expression of a polynucleotide” indicates that the detection of the presence of nucleic acids, the same or related to a nucleic acid sequence encoding NTAP, by Northern analysis is indicative of the presence of nucleic acids encoding NTAP in a sample, and thereby correlates with expression of the transcript from the polynucleotide encoding NTAP.

A “deletion,” as the term is used herein, refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term “derivative,” as used herein, refers to the chemical modification of a polypeptide sequence, or a polynucleotide sequence. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

The term “similarity,” as used herein, refers to a degree of complementarity. There may be partial similarity or complete similarity. The word “identity” may substitute for the word “similarity.” A partially complementary sequence that at least partially inhibits an identical sequence from hybridizing to a target nucleic acid is referred to as “substantially similar.” The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or Northern blot, solution hybridization, and the like) under conditions of reduced stringency. A substantially similar sequence or hybridization probe will compete for and inhibit the binding of a completely similar (identical) sequence to the target sequence under conditions of reduced stringency. This is not to say that conditions of reduced stringency are such that non-specific binding is permitted, as reduced stringency conditions require that the binding of two sequences to one another be a specific (i.e., a selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% similarity or identity). In the absence of non-specific binding, the substantially similar sequence or probe will not hybridize to the second non-complementary target sequence.

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The phrases "percent identity" or "% identity" refer to the percentage of sequence similarity found in a comparison of two or more amino acid or nucleic acid sequences. Percent identity can be determined electronically, e.g., by using the MegAlign™ program (DNASTAR, Inc., Madison WI). The MegAlign™ program can create alignments between two or more

5 sequences according to different methods, e.g., the clustal method. (See, e.g., Higgins, D.G. and P.M. Sharp (1988) Gene 73:237-244.) The clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. The percentage similarity between two amino acid sequences, e.g., sequence A and sequence B, is calculated by dividing the length of sequence A, minus the number of gap residues in sequence A,

10 minus the number of gap residues in sequence B, into the sum of the residue matches between sequence A and sequence B, times one hundred. Gaps of low or of no similarity between the two amino acid sequences are not included in determining percentage similarity. Percent identity between nucleic acid sequences can also be counted or calculated by other methods known in the art, e.g., the Jotun Hein method. (See, e.g., Hein, J. (1990) Methods Enzymol. 183:626-645.)

15 Identity between sequences can also be determined by other methods known in the art, e.g., by varying hybridization conditions.

"Human artificial chromosomes" (HACs), as described herein, are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the elements required for stable mitotic chromosome segregation and maintenance.

20 (See, e.g., Harrington, J.J. et al. (1997) Nat Genet. 15:345-355.)

The term "humanized antibody," as used herein, refers to antibody molecules in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

"Hybridization," as the term is used herein, refers to any process by which a strand of

25 nucleic acid binds with a complementary strand through base pairing.

As used herein, the term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C₀t or R₀t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence

30 immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" or "addition," as used herein, refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively, to the sequence found in the naturally occurring molecule.

35 "Immune response" can refer to conditions associated with inflammation, trauma, immune

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disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

The term "microarray," as used herein, refers to an arrangement of distinct
5 polynucleotides arrayed on a substrate, e.g., paper, nylon or any other type of membrane, filter, chip, glass slide, or any other suitable solid support.

The terms "element" or "array element" as used herein in a microarray context, refer to hybridizable polynucleotides arranged on the surface of a substrate.

The term "modulate," as it appears herein, refers to a change in the activity of NTAP. For
10 example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of NTAP.

The phrases "nucleic acid" or "nucleic acid sequence," as used herein, refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded
15 and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material. In this context, "fragments" refers to those nucleic acid sequences which, comprise a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:7-12, for example, as distinct from any other sequence in the same genome. For example, a fragment of SEQ ID NO:7-12 is useful in hybridization and amplification technologies
20 and in analogous methods that distinguish SEQ ID NO:7-12 from related polynucleotide sequences. A fragment of SEQ ID NO:7-12 is at least about 15-20 nucleotides in length. The precise length of the fragment of SEQ ID NO:7-12 and the region of SEQ ID NO:7-12 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment. In some cases, a fragment, when translated, would produce
25 polypeptides retaining some functional characteristic, e.g., antigenicity, or structural domain characteristic, e.g., ATP-binding site, of the full-length polypeptide.

The terms "operably associated" or "operably linked," as used herein, refer to functionally related nucleic acid sequences. A promoter is operably associated or operably linked with a coding sequence if the promoter controls the translation of the encoded polypeptide. While
30 operably associated or operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements, e.g., repressor genes, are not contiguously linked to the sequence encoding the polypeptide but still bind to operator sequences that control expression of the polypeptide.

The term "oligonucleotide," as used herein, refers to a nucleic acid sequence of at least
35 about 6 nucleotides to 60 nucleotides, preferably about 15 to 30 nucleotides, and most preferably

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about 20 to 25 nucleotides, which can be used in PCR amplification or in a hybridization assay or microarray. As used herein, the term "oligonucleotide" is substantially equivalent to the terms "amplimer," "primer," "oligomer," and "probe," as these terms are commonly defined in the art.

5 "Peptide nucleic acid" (PNA), as used herein, refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell. (See, e.g., Nielsen, P.E. et al. (1993) Anticancer Drug Des. 8:53-63.)

10 The term "sample," as used herein, is used in its broadest sense. A biological sample suspected of containing nucleic acids encoding NTAP, or fragments thereof, or NTAP itself, may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a solid support; a tissue; a tissue print; etc.

15 As used herein, the terms "specific binding" or "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, or an antagonist. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing the epitope A, or the presence
20 of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

As used herein, the term "stringent conditions" refers to conditions which permit hybridization between polynucleotides and the claimed polynucleotides. Stringent conditions can be defined by salt concentration, the concentration of organic solvent, e.g., formamide,
25 temperature, and other conditions well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature.

The term "substantially purified," as used herein, refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are
30 at least about 60% free, preferably about 75% free, and most preferably about 90% free from other components with which they are naturally associated.

A "substitution," as used herein, refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

"Transformation," as defined herein, describes a process by which exogenous DNA enters
35 and changes a recipient cell. Transformation may occur under natural or artificial conditions

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according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, viral infection, electroporation, heat shock, lipofection, and particle

- 5 bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

- A "variant" of NTAP polypeptides, as used herein, refers to an amino acid sequence that
10 is altered by one or more amino acid residues. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties (e.g., replacement of leucine with isoleucine). More rarely, a variant may have "nonconservative" changes (e.g., replacement of glycine with tryptophan). Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be
15 substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE™ software (DNASTAR).

- The term "variant," when used in the context of a polynucleotide sequence, may encompass a polynucleotide sequence related to NTAP. This definition may also include, for
20 example, "allelic" (as defined above), "splice," "species," or "polymorphic" variants. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or an absence of domains. Species variants are polynucleotide sequences that vary from one species to another. The resulting
25 polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for
30 a disease state.

THE INVENTION

The invention is based on the discovery of new human neurotransmission associated proteins (NTAP), the polynucleotides encoding NTAP, and the use of these compositions for the

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diagnosis, treatment, or prevention of cancer and immune and neurological disorders.

Table 1 shows the Clone ID of the Incyte Clone in which nucleic acids encoding each NTAP were first identified, and the Incyte clones (and libraries) and shotgun sequences which are part of the consensus nucleotide sequence of each NTAP. Table 2 shows various properties of the polypeptides of the invention and methods used to identify the protein through sequence homologies and protein motifs. Table 3 shows the tissue expression of each nucleic acid sequence by northern analysis and diseases or disorders associated with this tissue expression.

The following represent unique fragments of the nucleotide sequences encoding NTAP and useful, for example, as hybridization probes: the fragment of SEQ ID NO:7 from about nucleotide 568 to about nucleotide 711; the fragment of SEQ ID NO:8 from about nucleotide 435 to about nucleotide 479; the fragment of SEQ ID NO:9 from about nucleotide 335 to about nucleotide 388; the fragment of SEQ ID NO:10 from about nucleotide 393 to about nucleotide 452; the fragment of SEQ ID NO:11 from about nucleotide 758 to about nucleotide 799; and the fragment of SEQ ID NO:12 from about nucleotide 325 to about nucleotide 378.

The invention also encompasses NTAP variants. A preferred NTAP variant is one which has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% amino acid sequence identity to the NTAP amino acid sequence, and which contains at least one functional or structural characteristic of NTAP.

The invention also encompasses polynucleotides which encode NTAP. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:7-12, which encodes an NTAP

The invention also encompasses a variant of a polynucleotide sequence encoding NTAP. In particular, such a variant polynucleotide sequence will have at least about 80%, more preferably at least about 90%, and most preferably at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding NTAP. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:7-12 which has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:7-12. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of NTAP.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding NTAP, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide

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sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring NTAP, and all such variations are to be considered as being specifically disclosed.

5 Although nucleotide sequences which encode NTAP and its variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring NTAP under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding NTAP possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of
10 the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding NTAP and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

15 The invention also encompasses production of DNA sequences which encode NTAP and NTAP derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding NTAP or any fragment thereof.

20 Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:7-12 or fragments thereof, under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) For example, stringent salt concentration will ordinarily be less than about 750 mM
25 NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and most preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, while high stringency hybridization can be obtained in the presence of at least about 35% formamide, and most preferably at least about 50% formamide. Stringent temperature conditions will
30 ordinarily include temperatures of at least about 30°C, more preferably of at least about 37°C, and most preferably of at least about 42°C. Varying additional parameters, such as hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Various levels of stringency are accomplished by combining these various conditions as needed. In a preferred embodiment,
35 hybridization will occur at 30°C in 750 mM NaCl, 75 mM trisodium citrate, and 1% SDS. In a

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more preferred embodiment, hybridization will occur at 37°C in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 µg/ml denatured salmon sperm DNA (ssDNA). In a most preferred embodiment, hybridization will occur at 42°C in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50 % formamide, and 200 µg/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

The washing steps which follow hybridization can also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include temperature of at least about 25°C, more preferably of at least about 42°C, and most preferably of at least about 68°C. In a preferred embodiment, wash steps will occur at 25°C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a most preferred embodiment, wash steps will occur at 68°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art.

Methods for DNA sequencing and analysis are well known in the art. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE® (Amersham Pharmacia Biotech Ltd., Uppsala, Sweden), Taq polymerase (Perkin-Elmer), thermostable T7 polymerase (Amersham Pharmacia Biotech Ltd., Uppsala, Sweden), or combinations of polymerases and proofreading exonucleases, such as those found in the ELONGASE™ amplification system (Life Technologies, Inc., Rockville, MD). Preferably, sequence preparation is automated with machines, e.g., the ABI CATALYST™ 800 (Perkin-Elmer) or MICROLAB® 2200 (Hamilton Co., Reno, NV) systems, in combination with thermal cyclers. Sequencing can also be automated, such as by ABI PRISM™ 373 or 377 systems (Perkin-Elmer) or the MEGABACE™ 1000 capillary electrophoresis system (Molecular Dynamics, Inc., Sunnyvale, CA). Sequences can be analyzed using computer programs and algorithms well known in the art. (See, e.g., Ausubel, F. M. et al. (1997) Current Protocols in Molecular Biology, John Wiley & Sons, New York, NY, unit 7.7; and Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, Inc, New York, NY.)

The nucleic acid sequences encoding NTAP may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence

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from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR.

10 Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-306). Additionally, one may use PCR, nested primers, and PromoterFinder™ libraries (Clontech, Palo Alto, CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO™ 4.06 Primer Analysis software (National Biosciences Inc., Plymouth, MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., Genotyper™ and Sequence Navigator™ (Perkin-Elmer Corp.), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode NTAP may be cloned in recombinant DNA molecules that direct expression of NTAP, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the

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same or a functionally equivalent amino acid sequence may be produced and used to express NTAP.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter NTAP-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

In another embodiment, sequences encoding NTAP may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucl. Acids Res. Symp. Ser. 215-223, and Horn, T. et al. (1980) Nucl. Acids Res. Symp. Ser. 225-232.) Alternatively, NTAP itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solid-phase techniques. (See, e.g., Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A Peptide Synthesizer (Perkin-Elmer Corp.). Additionally, the amino acid sequence of NTAP, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) Methods Enzymol. 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman and Co., New York, NY.)

In order to express a biologically active NTAP, the nucleotide sequences encoding NTAP or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding NTAP. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding NTAP. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding NTAP and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where

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only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding NTAP and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, NY, ch. 4, 8, and 16-17; and Ausubel, F.M. et al. (1995, and periodic supplements) Current Protocols in Molecular Biology, John Wiley & Sons, New York, NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding NTAP. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus (CaMV) or tobacco mosaic virus (TMV)) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding NTAP. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding NTAP can be achieved using a multifunctional E. coli vector such as Bluescript® (Stratagene) or pSport1™ plasmid (GIBCO BRL). Ligation of sequences encoding NTAP into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509.) When large quantities of NTAP are needed, e.g. for the production of antibodies, vectors which direct high level expression of NTAP may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of NTAP. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH,

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may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, supra; and Grant et al. (1987) *Methods Enzymol.* 153:516-54; Scorer, C. A. et al. (1994) *Bio/Technology* 5 12:181-184.)

Plant systems may also be used for expression of NTAP. Transcription of sequences encoding NTAP may be driven viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV. (Takamatsu, N. (1987) *EMBO J.* 6:307-311.) Alternatively, plant promoters such as the small subunit of RUBISCO or 10 heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., Hobbs, S. or Murry, L.E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, NY; pp. 15 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding NTAP may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to 20 obtain infective virus which expresses NTAP in host cells. (See, e.g., Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments 25 of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes.

For long term production of recombinant proteins in mammalian systems, stable expression of NTAP in cell lines is preferred. For example, sequences encoding NTAP can be 30 transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of 35 cells which successfully express the introduced sequences. Resistant clones of stably transformed

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cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk* or *ap^r* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; and Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* or *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. 77:3567-3570; Colbere-Garapin, F. et al (1981) J. Mol. Biol. 150:1-14; and Murry, supra.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP) (Clontech), β glucuronidase and its substrate β -D-glucuronoside, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. et al. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding NTAP is inserted within a marker gene sequence, transformed cells containing sequences encoding NTAP can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding NTAP under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding NTAP and that express NTAP may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of NTAP using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on NTAP is preferred, but a

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competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St Paul, MN, Section IV; Coligan, J. E. et al. (1997 and periodic supplements) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York, NY; and Maddox, D.E. et al. (1983) J. Exp. Med. 158:1211-1216).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding NTAP include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding NTAP, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison, WI), and U.S. Biochemical Corp. (Cleveland, OH). Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding NTAP may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode NTAP may be designed to contain signal sequences which direct secretion of NTAP through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC, Manassas, VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding NTAP may be ligated to a heterologous sequence resulting in translation of a

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fusion protein in any of the aforementioned host systems. For example, a chimeric NTAP protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of NTAP activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the NTAP encoding sequence and the heterologous protein sequence, so that NTAP may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel, F. M. et al. (1995 and periodic supplements) Current Protocols in Molecular Biology, John Wiley & Sons, New York, NY, ch 10. A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled NTAP may be achieved in vitro using the TNT™ rabbit reticulocyte lysate or wheat germ extract systems (Promega, Madison, WI). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, preferably ³⁵S-methionine.

Fragments of NTAP may be produced not only by recombinant production, but also by direct peptide synthesis using solid-phase techniques. (See, e.g., Creighton, supra pp. 55-60.) Protein synthesis may be performed by manual techniques or by automation. Automated synthesis may be achieved, for example, using the Applied Biosystems 431A Peptide Synthesizer (Perkin-Elmer Corp.). Various fragments of NTAP may be synthesized separately and then combined to produce the full length molecule.

THERAPEUTICS

Partial chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of NTAP and various known neurotransmission associated proteins. In addition, NTAP is expressed in cancer and immortalized cell lines, and in inflammation and the immune response. Therefore, NTAP appears to play a role in cancer, and immune and neurological disorders.

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Therefore, in one embodiment, NTAP or a fragment or derivative thereof may be administered to a subject to treat or prevent a neurological disorder. Such disorders can include, but are not limited to, akathesia, Alzheimer's disease, amnesia, amyotrophic lateral sclerosis, bipolar disorder, catatonia, cerebral neoplasms, dementia, depression, diabetic neuropathy, Down's syndrome, tardive dyskinesia, dystonias, epilepsy, Huntington's disease, peripheral neuropathy, multiple sclerosis, neurofibromatosis, Parkinson's disease, paranoid psychoses, postherpetic neuralgia, schizophrenia, and Tourette's disorder.

In another embodiment, a vector capable of expressing NTAP or a fragment or derivative thereof may be administered to a subject to treat or prevent a neurological disorder including, but not limited to, those described above.

In a further embodiment, a pharmaceutical composition comprising a substantially purified NTAP in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a neurological disorder including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of NTAP may be administered to a subject to treat or prevent a neurological disorder including, but not limited to, those listed above.

In a further embodiment, an antagonist of NTAP may be administered to a subject to treat or prevent a cancer. Such a cancer may include, but is not limited to, adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus. In one aspect, an antibody which specifically binds NTAP may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express NTAP.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding NTAP may be administered to a subject to treat or prevent a cancer including, but not limited to, those described above.

In a further embodiment, an antagonist of NTAP may be administered to a subject to treat or prevent an immune disorder. Such a disorder may include, but is not limited to, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia

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with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's
 5 syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma.

In an additional embodiment, a vector expressing the complement of the polynucleotide
 10 encoding NTAP may be administered to a subject to treat or prevent an immune disorder including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination
 15 therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of NTAP may be produced using methods which are generally known in the
 20 art. In particular, purified NTAP may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind NTAP. Antibodies to NTAP may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments,
 25 and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are especially preferred for therapeutic use.

For the production of polyclonal antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with NTAP or with any fragment or oligopeptide thereof which has immunogenic properties. Rats and mice are preferred hosts for
 30 downstream applications involving monoclonal antibody production. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and
 35 Corynebacterium parvum are especially preferable. (For review of methods for antibody

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production and analysis, see, e.g., Harlow, E. and Lane, D. (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.)

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to NTAP have an amino acid sequence consisting of at least about 5 amino acids, and, more preferably, of at least about 14 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein and contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of NTAP amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to NTAP may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) *Nature* 256:495-497; Kozbor, D. et al. (1985) *J. Immunol. Methods* 81:31-42; Cote, R.J. et al. (1983) *Proc. Natl. Acad. Sci.* 80:2026-2030; and Cole, S.P. et al. (1984) *Mol. Cell Biol.* 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) *Proc. Natl. Acad. Sci.* 81:6851-6855; Neuberger, M.S. et al. (1984) *Nature* 312:604-608; and Takeda, S. et al. (1985) *Nature* 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce NTAP-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton D.R. (1991) *Proc. Natl. Acad. Sci.* 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) *Proc. Natl. Acad. Sci.* 86: 3833-3837; and Winter, G. et al. (1991) *Nature* 349:293-299.)

Antibody fragments which contain specific binding sites for NTAP may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) *Science* 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the

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desired specificity and minimal cross-reactivity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between NTAP and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering NTAP epitopes is preferred, but a competitive binding assay may also be employed. (Maddox, supra.)

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for NTAP. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of NTAP-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple NTAP epitopes, represents the average affinity, or avidity, of the antibodies for NTAP. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular NTAP epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the NTAP-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of NTAP, preferably in active form, from the antibody. (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington, D. C.; and Liddell, J. E. and Cryer, A. (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York, NY.)

The titre and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is preferred for use in procedures requiring precipitation of NTAP-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding NTAP, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, the complement of the polynucleotide encoding NTAP may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding NTAP. Thus, complementary molecules or fragments may be used to modulate NTAP activity, or to achieve regulation of gene function. Such technology is now well known in the art, and sense or antisense oligonucleotides or larger

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fragments can be designed from various locations along the coding or control regions of sequences encoding NTAP.

Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. Methods which are well known to those skilled in the art can be used to construct vectors to express nucleic acid sequences complementary to the polynucleotides encoding NTAP. (See, e.g., Sambrook, supra; and Ausubel, supra.)

Genes encoding NTAP can be turned off by transforming a cell or tissue with expression vectors which express high levels of a polynucleotide, or fragment thereof, encoding NTAP. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector, and may last even longer if appropriate replication elements are part of the vector system.

As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5', or regulatory regions of the gene encoding NTAP. Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, are preferred. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing Co., Mt. Kisco, NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding NTAP.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable.

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The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These
5 include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding NTAP. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA,
10 constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs
15 and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

Many methods for introducing vectors into cells or tissues are available and equally
20 suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nature Biotechnology 15:462-466.)

25 Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

An additional embodiment of the invention relates to the administration of a pharmaceutical or sterile composition, in conjunction with a pharmaceutically acceptable carrier,
30 for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of NTAP, antibodies to NTAP, and mimetics, agonists, antagonists, or inhibitors of NTAP. The compositions may be administered alone or in combination with at least one other agent, such as a stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water. The compositions
35 may be administered to a patient alone, or in combination with other agents, drugs, or hormones.

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The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

5 In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing Co., Easton, PA).

10 Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

15 Pharmaceutical preparations for oral use can be obtained through combining active compounds with solid excipient and processing the resultant mixture of granules (optionally, after grinding) to obtain tablets or dragee cores. Suitable auxiliaries can be added, if desired. Suitable excipients include carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, and sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as
20 methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums, including arabic and tragacanth; and proteins, such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, and alginic acid or a salt thereof, such as sodium alginate.

Dragee cores may be used in conjunction with suitable coatings, such as concentrated
25 sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules made of
30 gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with fillers or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

35 Pharmaceutical formulations suitable for parenteral administration may be formulated in

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aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be

5 prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils, such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate, triglycerides, or liposomes. Non-lipid polycationic amino polymers may also be used for delivery. Optionally, the suspension may also contain suitable stabilizers or agents to increase the solubility of the compounds and allow for the preparation of highly concentrated solutions.

10 For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

15 The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, and succinic acid. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1 mM to 50 mM histidine, 0.1% to 2%
20 sucrose, and 2% to 7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of NTAP, such labeling would include amount, frequency, and method of administration.

25 Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially either in
30 cell culture assays, e.g., of neoplastic cells or in animal models such as mice, rats, rabbits, dogs, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example
35 NTAP or fragments thereof, antibodies of NTAP, and agonists, antagonists or inhibitors of NTAP,

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which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of therapeutic to toxic effects is the therapeutic index, and it can be expressed as the ED_{50}/LD_{50} ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about $0.1 \mu g$ to $100,000 \mu g$, up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind NTAP may be used for the diagnosis of disorders characterized by expression of NTAP, or in assays to monitor patients being treated with NTAP or agonists, antagonists, or inhibitors of NTAP. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for NTAP include methods which utilize the antibody and a label to detect NTAP in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known

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in the art and may be used.

A variety of protocols for measuring NTAP, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of NTAP expression. Normal or standard values for NTAP expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody to NTAP under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, preferably by photometric means. Quantities of NTAP expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding NTAP may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which expression of NTAP may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of NTAP, and to monitor regulation of NTAP levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding NTAP or closely related molecules may be used to identify nucleic acid sequences which encode NTAP. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low), will determine whether the probe identifies only naturally occurring sequences encoding NTAP, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and should preferably have at least 50% sequence identity to any of the NTAP encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from a sequence selected from the group consisting of SEQ ID NO:7-12 or from genomic sequences including promoters, enhancers, and introns of the NTAP gene.

Means for producing specific hybridization probes for DNAs encoding NTAP include the cloning of polynucleotide sequences encoding NTAP or NTAP derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels,

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such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding NTAP may be used for the diagnosis of a disorder associated with expression of NTAP. Examples of such a disorder include, but are not limited to, a neurological disorder such as akathisia, Alzheimer's disease, amnesia, amyotrophic lateral sclerosis, bipolar disorder, catatonia, cerebral neoplasms, dementia, depression, diabetic neuropathy, Down's syndrome, tardive dyskinesia, dystonias, epilepsy, Huntington's disease, peripheral neuropathy, multiple sclerosis, neurofibromatosis, Parkinson's disease, paranoid psychoses, postherpetic neuralgia, schizophrenia, and Tourette's disorder; a cancer such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; and an immune disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma.. The polynucleotide sequences encoding NTAP may be used in Southern or Northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and ELISA assays; and in microarrays utilizing fluids or tissues from patients to detect altered NTAP expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding NTAP may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding NTAP may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the patient sample is significantly

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altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding NTAP in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

5 In order to provide a basis for the diagnosis of a disorder associated with expression of NTAP, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding NTAP, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from
10 normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated,
15 hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of a relatively high amount of transcript in biopsied
20 tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

25 Additional diagnostic uses for oligonucleotides designed from the sequences encoding NTAP may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding NTAP, or a fragment of a polynucleotide complementary to the polynucleotide encoding NTAP, and will be employed under optimized conditions for
30 identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantitation of closely related DNA or RNA sequences.

Methods which may also be used to quantitate the expression of NTAP include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol.
35 Methods 159:235-244; and Duplaa, C. et al. (1993) Anal. Biochem. 229-236.) The speed of

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quantitation of multiple samples may be accelerated by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as targets in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously and to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, and to develop and monitor the activities of therapeutic agents.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

In another embodiment of the invention, nucleic acid sequences encoding NTAP may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, R.A. (ed.) Molecular Biology and Biotechnology, VCH Publishers New York, NY, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) site. Correlation between the location of the gene encoding NTAP on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The nucleotide sequences of the invention may be used to detect differences in gene sequences among normal, carrier, and affected individuals.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms by physical

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mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or syndrome has been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, NTAP, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between NTAP and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The test compounds are reacted with NTAP, or fragments thereof, and washed. Bound NTAP is then detected by methods well known in the art. Purified NTAP can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding NTAP specifically compete with a test compound for binding NTAP. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with NTAP.

In additional embodiments, the nucleotide sequences which encode NTAP may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/091,677, are hereby expressly incorporated by reference.

35

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from CLONTECH Laboratories, Inc. or isolated from tissues described in Table 4. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIzol™ (Life Technologies, Inc.), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A⁺) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX™ latex particles (QIAGEN Inc., Valencia, CA), or an OLIGOTEX™ mRNA purification kit (QIAGEN Inc.). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE™ mRNA purification kit (Ambion, Austin, TX).

In some cases, Stratagene, Inc. (La Jolla, CA), was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP™ vector system (Stratagene, Inc.) or SUPERScript™ plasmid system (Life Technologies, Inc.), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, supra, 1997, units 5.1-6.6) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL® S1000, SEPHAROSE® CL2B, or SEPHAROSE® CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., pBLUESCRIPT® plasmid (Stratagene, Inc.), pSPORT™ 1 plasmid (Life Technologies, Inc.), or pINCY (Incyte Pharmaceuticals, Inc., Palo Alto, CA). Recombinant plasmids were transformed into competent *E. coli* cells, e.g., the XL1-Blue, XL1-BlueMRF, or SOLR™ strains (Stratagene, Inc.), or DH5α™, DH10B, or ElectroMAX DH10B competent cells (Life Technologies, Inc.).

II. Isolation of cDNA Clones

Plasmids were recovered from host cells by in vivo excision, using the UNIZAP™ vector system (Stratagene, Inc.), or by cell lysis. Plasmids were purified using at least one of the

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following: a Magic or WIZARD® Minipreps DNA purification system (Promega Corp.); an AGTC® Miniprep purification kit (Edge Biosystems, Gaithersburg, MD); the QIAWELL® 8 Plasmid, QIAWELL® 8 Plus Plasmid, or the QIAWELL® 8 Ultra Plasmid purification systems (QIAGEN Inc.); or the R.E.A.L.™ Prep 96 plasmid kit (QIAGEN Inc.). Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format. (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN® dye (Molecular Probes, Inc., Eugene, OR) and a Fluoroskan II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

The cDNAs were prepared for sequencing using either an ABI CATALYST 800 (Perkin-Elmer) or a MICROLAB® 2200 (Hamilton) sequencing preparation system in combination with Peltier PTC-200 thermal cyclers (MJ Research, Inc., Watertown, MA). The cDNAs were sequenced using the ABI PRISM™ 373 or 377 sequencing systems and ABI protocols, base calling software, and kits (Perkin-Elmer). Alternatively, solutions and dyes from Amersham Pharmacia Biotech, Ltd. were used in place of the ABI kits. In some cases, reading frames were determined using standard methods (Ausubel, supra). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example V.

The polynucleotide sequences derived from cDNA, extension, and shotgun sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the software programs used, corresponding algorithms, references, and cutoff parameters used where applicable. The references cited in the third column of Table 5 are incorporated by reference herein. Sequences were analyzed using MACDNASIS PRO software (Hitachi Software Engineering Co.) and LASERGENE software (DNASTAR Inc.).

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases such as GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS to acquire annotation, using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and were screened

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for open reading frames using programs based on GeneMark, BLAST, and FASTA. This was followed by translation of the full length polynucleotide sequences to derive the corresponding full length amino acid sequences. These full length polynucleotide and amino acid sequences were subsequently analyzed by querying against databases such as the GenBank databases described above and SwissProt, BLOCKS, PRINTS, PFAM, and Prosite.

IV. Northern Analysis

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; and Ausubel, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in nucleotide databases such as GenBank or LIFESEQ® database (Incyte Pharmaceuticals). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar.

The basis of the search is the product score, which is defined as:

$$\frac{\% \text{ sequence identity} \times \% \text{ maximum BLAST score}}{100}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1% to 2% error; and, with a product score of 70, the match will be exact. Similar molecules are usually identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

The results of Northern analysis are reported as a list of libraries in which the transcript encoding NTAP occurs. Abundance and percent abundance are also reported. Abundance directly reflects the number of times a particular transcript is represented in a cDNA library, and percent abundance is abundance divided by the total number of sequences examined in the cDNA library.

V. Extension of NTAP Encoding Polynucleotides

Full-length nucleic acid sequences (SEQ ID NO:7-12) were produced by extension of the component fragments described in Table 1, Column 5, using oligonucleotide primers based on those fragments. For each nucleic acid sequence, one primer was synthesized to initiate extension of an antisense polynucleotide, and the other was synthesized to initiate extension of a sense polynucleotide. Primers were used to facilitate the extension of the known sequence "outward" generating amplicons containing new unknown nucleotide sequence for the region of interest. The

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initial primers were designed from the cDNA using OLIGO™ 4.06 (National Biosciences, Plymouth, MN), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension is necessary or desired, additional sets of primers are designed to further extend the known region.

High fidelity amplification was obtained by following the instructions for the XL-PCR™ kit (Perkin-Elmer Corp.) and thoroughly mixing the enzyme and reaction mix. PCR was performed using the PTC-200 thermal cycler (MJ Research, Inc.), beginning with 40 pmol of each primer and the recommended concentrations of all other components of the kit, with the following parameters:

	Step 1	94° C for 1 min (initial denaturation)
15	Step 2	65° C for 1 min
	Step 3	68° C for 6 min
	Step 4	94° C for 15 sec
	Step 5	65° C for 1 min
	Step 6	68° C for 7 min
20	Step 7	Repeat steps 4 through 6 for an additional 15 cycles
	Step 8	94° C for 15 sec
	Step 9	65° C for 1 min
	Step 10	68° C for 7:15 min
	Step 11	Repeat steps 8 through 10 for an additional 12 cycles
25	Step 12	72° C for 8 min
	Step 13	4° C (and holding)

A 5 µl to 10 µl aliquot of the reaction mixture was analyzed by electrophoresis on a low concentration (about 0.6% to 0.8%) agarose mini-gel to determine which reactions were successful in extending the sequence. Bands thought to contain the largest products were excised from the gel, purified using QIAQUICK™ kit (QIAGEN Inc.), and trimmed of overhangs using Klenow enzyme to facilitate religation and cloning.

After ethanol precipitation, the products were redissolved in 13 µl of ligation buffer, 1 µl T4-DNA ligase (15 units) and 1 µl T4 polynucleotide kinase were added, and the mixture was incubated at room temperature for 2 to 3 hours, or overnight at 16° C. Competent *E. coli* cells (in 40 µl of appropriate media) were transformed with 3 µl of ligation mixture and cultured in 80 µl of SOC medium. (See, e.g., Sambrook, *supra*, Appendix A, p. 2.) After incubation for one hour at 37°C, the *E. coli* mixture was plated on Luria Bertani (LB) agar (See, e.g., Sambrook, *supra*, Appendix A, p. 1) containing carbenicillin (2x carb). The following day, several colonies were

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randomly picked from each plate and cultured in 150 μ l of liquid LB/2x carb medium placed in an individual well of an appropriate commercially-available sterile 96-well microtiter plate. The following day, 5 μ l of each overnight culture was transferred into a non-sterile 96-well plate and, after dilution 1:10 with water, 5 μ l from each sample was transferred into a PCR array.

- 5 For PCR amplification, 18 μ l of concentrated PCR reaction mix (3.3x) containing 4 units of rTth DNA polymerase, a vector primer, and one or both of the gene specific primers used for the extension reaction were added to each well. Amplification was performed using the following conditions:

	Step 1	94° C for 60 sec
10	Step 2	94° C for 20 sec
	Step 3	55° C for 30 sec
	Step 4	72° C for 90 sec
	Step 5	Repeat steps 2 through 4 for an additional 29 cycles
	Step 6	72° C for 180 sec
15	Step 7	4° C (and holding)

Aliquots of the PCR reactions were run on agarose gels together with molecular weight markers. The sizes of the PCR products were compared to the original partial cDNAs, and appropriate clones were selected, ligated into plasmid, and sequenced.

- 20 In like manner, the nucleotide sequence of SEQ ID NO:7-12 are used to obtain 5' regulatory sequences using the procedure above, oligonucleotides designed for 5' extension, and an appropriate genomic library.

VI. Labeling and Use of Individual Hybridization Probes

- Hybridization probes derived from SEQ ID NO:7-12 are employed to screen cDNAs, 25 genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO™ 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ -³²P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase 30 (DuPont NEN®, Boston, MA). The labeled oligonucleotides are substantially purified using a Sephadex™ G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

- 35 The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham, NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature

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under increasingly stringent conditions up to 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. After XOMAT AR™ film (Kodak, Rochester, NY) is exposed to the blots to film for several hours, hybridization patterns are compared visually.

VII. Microarrays

- 5 A chemical coupling procedure and an ink jet device can be used to synthesize array elements on the surface of a substrate. (See, e.g., Baldeschweiler, supra.) An array analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced by hand or using available methods and machines and contain any appropriate number of elements.
- 10 After hybridization, nonhybridized probes are removed and a scanner used to determine the levels and patterns of fluorescence. The degree of complementarity and the relative abundance of each probe which hybridizes to an element on the microarray may be assessed through analysis of the scanned images.

- Full-length cDNAs, Expressed Sequence Tags (ESTs), or fragments thereof may
- 15 comprise the elements of the microarray. Fragments suitable for hybridization can be selected using software well known in the art such as LASERGENE™ software (DNASTAR). Full-length cDNAs, ESTs, or fragments thereof corresponding to one of the nucleotide sequences of the present invention, or selected at random from a cDNA library relevant to the present invention, are arranged on an appropriate substrate, e.g., a glass slide. The cDNA is fixed to the slide using, e.g.,
- 20 UV cross-linking followed by thermal and chemical treatments and subsequent drying. (See, e.g., Schena, M. et al. (1995) Science 270:467-470; and Shalon, D. et al. (1996) Genome Res. 6:639-645.) Fluorescent probes are prepared and used for hybridization to the elements on the substrate. The substrate is analyzed by procedures described above.

VIII. Complementary Polynucleotides

- 25 Sequences complementary to the NTAP-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring NTAP. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO™ 4.06 software and the coding sequence of NTAP. To inhibit
- 30 transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the NTAP-encoding transcript.

IX. Expression of NTAP

- Expression and purification of NTAP is achieved using bacterial or virus-based
- 35 expression systems. For expression of NTAP in bacteria, cDNA is subcloned into an appropriate

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vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express NTAP upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of NTAP in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding NTAP by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E. K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, NTAP is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Pharmacia, Piscataway, NJ). Following purification, the GST moiety can be proteolytically cleaved from NTAP at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak, Rochester, NY). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN Inc, Chatsworth, CA). Methods for protein expression and purification are discussed in Ausubel, F. M. et al. (1995 and periodic supplements) Current Protocols in Molecular Biology, John Wiley & Sons, New York, NY, ch 10, 16. Purified NTAP obtained by these methods can be used directly in the following activity assay.

30 X. Demonstration of NTAP Activity

NTAP, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton et al. (1973) Biochem. J. 133:529.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled NTAP, washed, and any wells with labeled NTAP complex are assayed. Data obtained using different concentrations of NTAP are used to calculate values for the number, affinity, and association of NTAP with the

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candidate molecules.

XI. Functional Assays

NTAP function is assessed by expressing the sequences encoding NTAP at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT™ plasmid (Life Technologies) and pCR™ 3.1 plasmid (Invitrogen, Carlsbad, CA) both of which contain the cytomegalovirus promoter. 5-10 µg of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2 µg of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP) (Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP, and to evaluate properties, for example, their apoptotic state. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York, NY.

The influence of NTAP on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding NTAP and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success, NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding NTAP and other genes of interest can be analyzed by Northern analysis or microarray techniques.

XII. Production of NTAP Specific Antibodies

NTAP substantially purified using polyacrylamide gel electrophoresis (PAGE)(see, e.g., Harrington, M.G. (1990) Methods Enzymol. 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

5 Alternatively, the NTAP amino acid sequence is analyzed using LASERGENE™ software (DNASTAR Inc.) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel supra, ch. 11.)

10 Typically, oligopeptides 15 residues in length are synthesized using an Applied Biosystems Peptide Synthesizer Model 431A using fmoc-chemistry and coupled to KLH (Sigma Aldrich, St. Louis, MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel supra.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for
15 anti-peptide activity by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XIII. Purification of Naturally Occurring NTAP Using Specific Antibodies

Naturally occurring or recombinant NTAP is substantially purified by immunoaffinity chromatography using antibodies specific for NTAP. An immunoaffinity column is constructed
20 by covalently coupling anti-NTAP antibody to an activated chromatographic resin, such as CNBr-activated Sepharose (Pharmacia & Upjohn). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing NTAP are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of NTAP (e.g., high ionic strength
25 buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/NTAP binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and NTAP is collected.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of
30 the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

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Table 1

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	7	238506	SINTNOT02	238506H1 (SINTNOT02), 881185R1 (THYRNOT02), 1809706F6 and 1809880T6 (PROSTUT12), 2371286F6 (ADREN07), 3558166H1 (LUNGNOT31)
2	8	414692	BRSTNOT01	030604F1 (THP1NOB01), 061690F1 (LUNGNOT01), 414692H1 (BRSTNOT01), 1533952F1 (SPLNNOT04)
3	9	998868	KIDNTUT01	484199H1 and 484199R6 (HNT2RAT01), 489188H1 (HNT2AGT01), 998868H1 (KIDNTUT01), 1944742R6 (PITUNOT01), 2206131F6 (SPLNFET02), 3509110H1 (CONCNOT01)
4	10	1296451	PGANNOT03	000531R7 (U937NOT01), 623274R6 (PGANNOT01), 1295462F1 (PGANNOT03), 1296451H1 (PGANNOT03), 1664686F6 (BRSTNOT09), 2824843H1 (ADRETUT06)
5	11	1739035	COLNNOT22	1469082F6 and 1469082T1 (PANCTUT02), 1665101H1 (BRSTNOT09), 1739035F6 and 1739035H1 (COLNNOT22), 1998944R6 (BRSTTUT03), 3770403H1 (BRSTNOT25)
6	12	2799056	NPOLNOT01	875877R1 (LUNGAST01), 1509734F1 (LUNGNOT14), 1979922R6, 1979922T6 and 1981971H1 (LUNGTUT03), 2799056H1 (NPOLNOT01), SAWA01057F1

Table 2

Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence	Identification	Analytical Methods
1	251	S88 S174 S191 T205 S25 T199			neuronal protein	BLAST
2	238	S11 S12 T105 T117 S145 S206 S61		S21-Q45	NMDA receptor	BLAST PRINTS
3	408	T8 S33 T220 S225 T289 S330 S331 S58 S200 T284 Y165 Y372	N31 N204		Benzodiazepine receptor- associated protein	BLAST
4	272	T2 S103 T126 T167 S177 S244		C43-C54 C74-C85 C139-C150	Putative mammalian homeotic protein	BLAST MOTIFS PRINTS BLOCKS
5	363	T192 T19 S65 S86 T213 T18 T47 S133 T159 T215 S253	N4 N14 N131 N251	P229-P240	rhodopsin	PRINTS
6	484	S102 T127 S298 T390 T140 S164 S404 Y236	N48 N264 N401		Putative odorant- binding protein	BLAST

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Table 3

Seq ID NO:	Tissue Expression (Fraction of Total)	Disease Class (Fraction of Total)	Vector
7	Reproductive (0.275) Hematopoietic/Immune (0.200) Gastrointestinal (0.175)	Cancer (0.400) Inflammation (0.375) Fetal (0.175)	pBluescript
8	Reproductive (0.272) Cardiovascular (0.140) Hematopoietic/Immune (0.132)	Cancer (0.439) Inflammation (0.281) Fetal (0.140)	pBluescript
9	Cardiovascular (0.200) Nervous (0.200) Developmental (0.133)	Fetal (0.467) Cancer (0.400) Inflammation (0.200)	pSPORT1
10	Nervous (0.278) Developmental (0.250) Reproductive (0.222)	Cancer (0.333) Fetal (0.333) Inflammation (0.167)	pINCY
11	Reproductive (0.381) Gastrointestinal (0.286) Developmental (0.119)	Cancer (0.548) Inflammation (0.261) Fetal (0.214)	pINCY
12	Cardiovascular (0.444) Reproductive (0.278) Developmental (0.167)	Cancer (0.667) Fetal (0.167) Inflammation (0.167)	pINCY

Table 4

Nucleotide SEQ ID NO:	Clone ID	Library	Library Comment
7	238506	SINTNOT02	Library was constructed using RNA isolated from the small intestine of a 55-year-old Caucasian female, who died from a subarachnoid hemorrhage. Serologies were positive for cytomegalovirus (CMV).
8	414692	BRSTNOT01	Library was constructed using RNA isolated from the breast tissue of a 56-year-old Caucasian female who died in a motor vehicle accident.
9	998868	KIDNTUT01	Library was constructed using RNA isolated from the kidney tumor tissue removed from an 8-month-old female during nephroureterectomy. Pathology indicated Wilms' tumor (nephroblastoma), which involved 90 percent of the renal parenchyma.
10	1296451	PGANNOT03	Library was constructed using RNA isolated from paraganglionic tumor tissue removed from the intra-abdominal region of a 46-year-old Caucasian male during exploratory laparotomy. Pathology indicated a benign paraganglioma and was associated with a grade 2 renal cell carcinoma, clear cell type, which did not penetrate the capsule.
11	1739035	COLNNOT22	Library was constructed using RNA isolated from colon tissue removed from a 56-year-old Caucasian female with Crohn's disease during a partial resection of the small intestine. Pathology indicated Crohn's disease of the ileum and ileal-colonic anastomosis, causing a fistula at the anastomotic site that extended into pericolonic fat. The ileal mucosa showed linear and punctate ulcers with intervening normal tissue.
12	2799056	NPOLNOT01	Library was constructed using RNA isolated from nasal polyp tissue removed from a 78-year-old Caucasian male during a nasal polypectomy. Pathology indicated a nasal polyp and striking eosinophilia. Patient history included asthma and nasal polyps.

TABLE 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25: 3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA includes five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183: 63-98; and Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: z-score = 10 or greater Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS and PRINTS databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S and J.G. Henikoff, Nucl. Acid Res., 19:6565-72, 1991. J.G. Henikoff and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37: 417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and Probability value= 1.0E-3 or less
PFAM	A Hidden Markov Models-based application useful for protein family search.	Krogh, A. et al. (1994) J. Mol. Biol., 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits, depending on individual protein families

TABLE 5 (con)

Program	Description	Reference	Parameter Threshold
GeneMark	A gene prediction algorithm that is based on inhomogeneous Markov chain models and is useful for DNA sequence analysis and particularly for gene prediction.	Borodovsky, M. and J. McIninch (1993) Computers Chem. 17: 123-133; Blattner, F.R. et al. (1993) Nucleic Acids Res. 21: 5408-5417.	Score= 0.4 or greater
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribkov, M. et al. (1988) CABIOS 4:61-66; Gribkov, et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25: 217-221.	Score= 4.0 or greater
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M. S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12: 431-439.	Score=5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch et al. <i>supra</i> ; Wisconsin Package Program Manual, version 9, page M51-59; Genetics Computer Group, Madison, WI.	

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What is claimed is:

1. A substantially purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6, and fragments thereof.
2. A substantially purified variant having at least 90% amino acid identity to the amino acid sequence of claim 1.
3. An isolated and purified polynucleotide encoding the polypeptide of claim 1.
4. An isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide of claim 3.
5. An isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide of claim 3.
6. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide sequence of claim 3.
7. An isolated and purified polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:12, and fragments thereof.
8. An isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide of claim 7.
9. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide of claim 7.
10. An expression vector comprising at least a fragment of the polynucleotide of claim 3.
11. A host cell comprising the expression vector of claim 10.

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12. A method for producing a polypeptide, the method comprising the steps of:
- a) culturing the host cell of claim 11 under conditions suitable for the expression of the polypeptide; and
 - b) recovering the polypeptide from the host cell culture.
13. A pharmaceutical composition comprising the polypeptide of claim 1 in conjunction with a suitable pharmaceutical carrier.
14. A purified antibody which specifically binds to the polypeptide of claim 1.
15. A purified agonist of the polypeptide of claim 1.
16. A purified antagonist of the polypeptide of claim 1.
17. A method for treating or preventing neurological disorder, the method comprising administering to a subject in need of such treatment an effective amount of the pharmaceutical composition of claim 13.
18. A method for treating or preventing a cancer, the method comprising administering to a subject in need of such treatment an effective amount of the antagonist of claim 16.
19. A method for treating or preventing an immune disorder, the method comprising administering to a subject in need of such treatment an effective amount of the antagonist of claim 16.
20. A method for detecting a polynucleotide, the method comprising the steps of:
- (a) hybridizing the polynucleotide of claim 6 to at least one of the nucleic acids in a biological sample, thereby forming a hybridization complex; and
 - (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of the polynucleotide encoding the polypeptide in the biological sample.
21. The method of claim 20 further comprising amplifying the polynucleotide prior to hybridization.

PCT

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International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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(21) International Application Number: PCT/US99/15121 (22) International Filing Date: 2 July 1999 (02.07.99) (30) Priority Data: 60/091,677 2 July 1998 (02.07.98) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Application US 60/091,677 (CIP) Filed on 2 July 1998 (02.07.98) (71) Applicant (for all designated States except US): INCYTE PHARMACEUTICALS, INC. [US/US]; 3174 Porter Drive, Palo Alto, CA 94304 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): LAL, Preeti [IN/US]; 2382 Lass Drive, Santa Clara, CA 95054 (US). TANG, Y., Tom [CN/US]; 4230 Ranwick Court, San Jose, CA 95118 (US). YUE, Henry [US/US]; 826 Lois Avenue, Sunnyvale, CA 94087 (US). CORLEY, Neil, C. [US/US]; 1240 Dale Avenue #30, Mountain View, CA 94040 (US). GUEGLER, Karl, J. [CH/US]; 1048 Oakland Avenue, Menlo Park, CA 94025 (US). GORGONE, Gina, A. [US/US]; 1253 Pinecrest		Drive, Boulder Creek, CA 95006 (US). BAUGHN, Mariah, R. [US/US]; 14244 Santiago Road, San Leandro, CA 94577 (US). PATTERSON, Chandra [US/US]; 490 Sherwood Way #1, Menlo Park, CA 94025 (US). (74) Agents: BILLINGS, Lucy, J. et al.; Incyte Pharmaceuticals, Inc., 3174 Porter Drive, Palo Alto, CA 94304 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: NEUROTRANSMISSION ASSOCIATED PROTEINS (57) Abstract The invention provides human neurotransmission associated proteins (NTAP) and polynucleotides which identify and encode NTAP. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating or preventing disorders associated with expression of NTAP.		

Docket No.: PF-0551 USN

DECLARATION AND POWER OF ATTORNEY FOR UNITED STATES PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,
and

I believe that I am the original, first and sole inventor (if only one name is listed below)
or an original, first and joint inventor (if more than one name is listed below) of the subject
matter which is claimed and for which a United States patent is sought on the invention entitled

NEUROTRANSMISSION ASSOCIATED PROTEINS

the specification of which:

 / / is attached hereto.

 / X / was filed on December 19, 2000 as application Serial No. 09/720,530 and if this box
contains an X / /, was amended on _____.

 / X / was filed as Patent Cooperation Treaty international application No. PCT/US99/15121
on July 2, 1999, if this box contains an X / /, was amended on under Patent Cooperation Treaty
Article 19 on _____ 2001, and if this box contains an X / /, was amended on _____.

I hereby state that I have reviewed and understand the contents of the above-identified
specification, including the claims, as amended by any amendment referred to above.

I acknowledge my duty to disclose information which is material to the examination of
this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim the benefit under Title 35, United States Code, §119 or §365(a)-(b) of any
foreign application(s) for patent or inventor's certificate indicated below and of any Patent
Cooperation Treaty international applications(s) designating at least one country other than the
United States indicated below and have also identified below any foreign application(s) for
patent or inventor's certificate and Patent Cooperation Treaty international application(s)
designating at least one country other than the United States for the same subject matter and
having a filing date before that of the application for said subject matter the priority of which is
claimed:

Country	Number	Filing Date	Priority Claimed
_____	_____	_____	// Yes // No
_____	_____	_____	// Yes // No

Docket No.: PF-0551 USN

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional application(s) listed below.

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
60/091,677	2 July 1998	Expired

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in said prior application(s) in the manner required by the first paragraph of Title 35, United States Code §112, I acknowledge my duty to disclose material information as defined in Title 37 Code of Federal Regulations, §1.56(a) which occurred between the filing date(s) of the prior application(s) and the national or Patent Cooperation Treaty international filing date of this application:

Application Serial No.	Filed	Status (Pending, Abandoned, Patented)
---------------------------	-------	--

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respectively and individually, as my patent attorneys and/or agents, with full power of substitution and revocation, to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith. Please address all communications to:

Docket No.: PF-0551 USN

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

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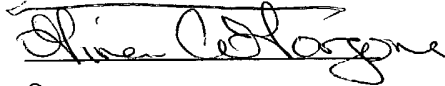
Docket No.: PF-0551 USN

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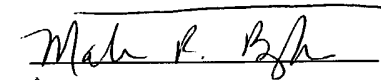
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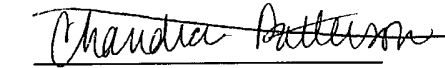
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PCT/US99/15121

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Lys	Asp	Leu	Met	Thr	Gln	Leu	Arg	Gln	Val	Leu	Glu	Ser	Arg	Leu					
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Gln	Arg	Pro	Leu	Pro	Glu	Asp	Leu	Ala	Glu	Ala	Leu	Ala	Ser	Gly					
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				140					145					150					

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Pro Phe Ile His Val	Pro Ser Pro Ala Val	Pro Lys Leu Ser Ala
155	160	165
Leu Lys Ala Arg Lys	Asn Val Glu Ser Phe	Leu Glu Ala Cys Arg
170	175	180
Lys Met Gly Val Pro	Glu Ala Asp Leu Cys	Ser Pro Ser Asp Leu
185	190	195
Leu Gln Gly Thr Ala	Arg Gly Leu Arg Thr	Ala Leu Glu Ala Val
200	205	210
Lys Arg Val Gly Gly	Lys Ala Leu Pro Pro	Leu Trp Pro Pro Ser
215	220	225
Gly Leu Gly Gly Phe	Val Val Phe Tyr Val	Val Leu Met Leu Leu
230	235	240
Leu Tyr Val Thr Tyr	Thr Arg Leu Leu Gly	Ser
245	250	

<210> 2

<211> 238

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 414692

<400> 2

Met Ala Asp Pro Asp	Pro Arg Tyr Pro Arg	Ser Ser Ile Glu Asp
1	5	10
Asp Phe Asn Tyr Gly	Ser Ser Val Ala Ser	Ala Thr Val His Ile
20	25	30
Arg Met Ala Phe Leu	Arg Lys Val Tyr Ser	Ile Leu Ser Leu Gln
35	40	45
Val Leu Leu Thr Thr	Val Thr Ser Thr Val	Phe Leu Tyr Phe Glu
50	55	60
Ser Val Arg Thr Phe	Val His Glu Ser Pro	Ala Leu Ile Leu Leu
65	70	75
Phe Ala Leu Gly Ser	Leu Gly Leu Ile Phe	Ala Leu Thr Leu Asn
80	85	90
Arg His Lys Tyr Pro	Leu Asn Leu Tyr Leu	Leu Phe Gly Phe Thr
95	100	105
Leu Leu Glu Ala Leu	Thr Val Ala Val Val	Val Thr Phe Tyr Asp
110	115	120
Val Tyr Ile Ile Leu	Gln Ala Phe Ile Leu	Thr Thr Thr Val Phe
125	130	135
Phe Gly Leu Thr Val	Tyr Thr Leu Gln Ser	Lys Lys Asp Phe Ser
140	145	150
Lys Phe Gly Ala Gly	Leu Phe Ala Leu Leu	Trp Ile Leu Cys Leu
155	160	165
Ser Gly Phe Leu Lys	Phe Phe Phe Tyr Ser	Glu Ile Met Glu Leu
170	175	180
Val Leu Ala Ala Ala	Gly Ala Leu Leu Phe	Cys Gly Phe Ile Ile
185	190	195
Tyr Asp Thr His Ser	Leu Met His Lys Leu	Ser Pro Glu Glu Tyr
200	205	210
Val Leu Ala Ala Ile	Ser Leu Tyr Leu Asp	Ile Ile Asn Leu Phe

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	215		220	225
Leu His Leu Leu Arg Phe Leu Glu Ala Val Asn Lys Lys				
	230		235	

<210> 3

<211> 408

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 998868

<400> 3

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Asp Val Leu Gly Asn Asp Arg Arg Arg Glu Trp Ala Ala Leu Gly		
20 25 30		
Asn Met Ser Lys Glu Asp Ala Met Val Glu Phe Val Lys Leu Leu		
35 40 45		
Asn Arg Cys Cys His Leu Phe Ser Thr Tyr Val Ala Ser His Lys		
50 55 60		
Ile Glu Lys Glu Glu Gln Asp Lys Lys Arg Gln Glu Glu Glu Glu		
65 70 75		
Arg Arg Arg Arg Glu Glu Glu Arg Glu Arg Leu Pro Lys Glu		
80 85 90		
Glu Glu Lys Arg Arg Arg Glu Glu Glu Glu Arg Leu Arg Arg Ala		
95 100 105		
Ala Glu Glu Arg Arg Arg Ile Glu Glu Glu Arg Leu Arg Leu Glu		
110 115 120		
Gln Gln Lys Gln Gln Ile Met Ala Ala Leu Asn Ser Gln Thr Ala		
125 130 135		
Val Gln Phe Gln Gln Tyr Ala Ala Gln Gln Tyr Pro Gly Asn Tyr		
140 145 150		
Glu Gln Gln Gln Ile Leu Ile Arg Gln Leu Gln Glu Gln His Tyr		
155 160 165		
Gln Gln Tyr Met Gln Gln Leu Tyr Gln Val Gln Leu Ala Gln Gln		
170 175 180		
Gln Ala Ala Leu Gln Lys Gln Gln Glu Val Val Val Ala Gly Ser		
185 190 195		
Ser Leu Pro Thr Ser Ser Lys Val Asn Ala Thr Val Pro Ser Asn		
200 205 210		
Met Met Ser Val Asn Gly Gln Ala Lys Thr His Thr Asp Ser Ser		
215 220 225		
Glu Lys Glu Leu Glu Pro Glu Ala Ala Glu Glu Ala Leu Glu Asn		
230 235 240		
Gly Pro Lys Glu Ser Leu Pro Val Ile Ala Ala Pro Ser Met Trp		
245 250 255		
Thr Arg Pro Gln Ile Lys Asp Phe Lys Glu Lys Ile Gln Gln Asp		
260 265 270		
Ala Asp Ser Val Ile Thr Val Gly Arg Gly Glu Val Val Thr Val		
275 280 285		
Arg Val Pro Thr His Glu Glu Gly Ser Tyr Leu Phe Trp Glu Phe		
290 295 300		

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Ala Thr Asp Asn Tyr Asp Ile Gly Phe Gly Val Tyr Phe Glu Trp		
	305	310 315
Thr Asp Ser Pro Asn Thr Ala Val Ser Val His Val Ser Glu Ser		
	320	325 330
Ser Asp Asp Asp Glu Glu Glu Glu Glu Asn Ile Gly Cys Glu Glu		
	335	340 345
Lys Ala Lys Lys Asn Ala Asn Lys Pro Leu Leu Asp Glu Ile Val		
	350	355 360
Pro Val Tyr Arg Arg Asp Cys His Glu Glu Val Tyr Ala Gly Ser		
	365	370 375
His Gln Tyr Pro Gly Arg Gly Val Tyr Leu Leu Lys Phe Asp Asn		
	380	385 390
Ser Tyr Ser Leu Trp Arg Ser Lys Ser Val Tyr Tyr Arg Val Tyr		
	395	400 405
Tyr Thr Arg		

<210> 4

<211> 272

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1296451

<400> 4

Met Thr Ala Thr Glu Ala Leu Leu Arg Val Leu Leu Leu Leu Leu		
1 5	10	15
Ala Phe Gly His Ser Thr Tyr Gly Ala Glu Cys Phe Pro Ala Cys		
20	25	30
Asn Pro Gln Asn Gly Phe Cys Glu Asp Asp Asn Val Cys Arg Cys		
35	40	45
Gln Pro Gly Trp Gln Gly Pro Leu Cys Asp Gln Cys Val Thr Ser		
50	55	60
Pro Gly Cys Leu His Gly Leu Cys Gly Glu Pro Gly Gln Cys Ile		
65	70	75
Cys Thr Asp Gly Trp Asp Gly Glu Leu Cys Asp Arg Asp Val Arg		
80	85	90
Ala Cys Ser Ser Ala Pro Cys Ala Asn Asn Gly Tyr Ser Gly Lys		
95	100	105
Asp Cys Gln Lys Lys Asp Gly Pro Cys Val Ile Asn Gly Ser Pro		
110	115	120
Cys Gln His Gly Gly Thr Cys Val Asp Asp Glu Gly Arg Ala Ser		
125	130	135
His Ala Ser Cys Leu Cys Pro Pro Gly Phe Ser Gly Asn Phe Cys		
140	145	150
Glu Ile Val Ala Ser Pro Cys Gln Asn Gly Gly Thr Cys Leu Gln		
155	160	165
His Thr Gln Pro Glu His Arg Ile Leu Lys Val Ser Met Lys Glu		
170	175	180
Leu Asn Lys Lys Thr Pro Leu Leu Thr Glu Gly Gln Ala Ile Cys		
185	190	195
Phe Thr Ile Leu Gly Val Leu Thr Ser Leu Val Val Leu Gly Thr		
200	205	210

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Val	Gly	Ile	Val	Phe	Leu	Asn	Lys	Cys	Glu	Thr	Trp	Val	Ser	Asn	
				215					220					225	
Leu	Arg	Tyr	Asn	His	Met	Leu	Arg	Lys	Lys	Lys	Asn	Leu	Leu	Leu	
				230					235					240	
Gln	Tyr	Asn	Ser	Gly	Glu	Asp	Leu	Ala	Val	Asn	Ile	Ile	Phe	Pro	
				245					250					255	
Glu	Lys	Ile	Asp	Met	Thr	Thr	Phe	Ser	Lys	Glu	Ala	Gly	Asp	Glu	
				260					265					270	
Glu	Ile														

<210> 5

<211> 363

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1739035

<400> 5

Met	Cys	Leu	Asn	His	Ser	Asn	Gln	Phe	Thr	Gln	Leu	Gly	Asn	Ile	
1				5					10					15	
Thr	Glu	Thr	Thr	Lys	Phe	Glu	Lys	Leu	Ala	Glu	Asp	Cys	Lys	Arg	
				20					25					30	
Ser	Met	Asp	Ile	Leu	Lys	Gln	Ala	Phe	Val	Arg	Gly	Leu	Pro	Thr	
				35					40					45	
Pro	Thr	Ala	Arg	Phe	Glu	Gln	Arg	Thr	Phe	Ser	Val	Ile	Lys	Ile	
				50					55					60	
Phe	Pro	Asp	Leu	Ser	Ser	Asn	Asp	Met	Leu	Leu	Phe	Ile	Val	Lys	
				65					70					75	
Gly	Ile	Asn	Leu	Pro	Thr	Pro	Pro	Gly	Leu	Ser	Pro	Gly	Asp	Leu	
				80					85					90	
Asp	Val	Phe	Val	Arg	Phe	Asp	Phe	Pro	Tyr	Pro	Asn	Val	Glu	Glu	
				95					100					105	
Ala	Gln	Lys	Asp	Lys	Thr	Ser	Val	Ile	Lys	Asn	Thr	Asp	Ser	Pro	
				110					115					120	
Glu	Phe	Lys	Glu	Gln	Phe	Lys	Leu	Cys	Ile	Asn	Arg	Ser	His	Arg	
				125					130					135	
Gly	Phe	Arg	Arg	Ala	Ile	Gln	Thr	Lys	Gly	Ile	Lys	Phe	Glu	Val	
				140					145					150	
Val	His	Lys	Gly	Gly	Leu	Phe	Lys	Thr	Asp	Arg	Val	Leu	Gly	Thr	
				155					160					165	
Ala	Gln	Leu	Lys	Leu	Asp	Ala	Leu	Glu	Ile	Ala	Cys	Glu	Val	Arg	
				170					175					180	
Glu	Ile	Leu	Glu	Val	Leu	Asp	Gly	Arg	Arg	Pro	Thr	Gly	Gly	Arg	
				185					190					195	
Leu	Glu	Val	Met	Val	Arg	Ile	Arg	Glu	Pro	Leu	Thr	Ala	Gln	Gln	
				200					205					210	
Leu	Glu	Thr	Thr	Thr	Glu	Arg	Trp	Leu	Val	Ile	Asp	Pro	Val	Pro	
				215					220					225	
Ala	Ala	Val	Pro	Thr	Gln	Val	Ala	Gly	Pro	Lys	Gly	Lys	Ala	Pro	
				230					235					240	
Pro	Val	Pro	Ala	Pro	Ala	Arg	Glu	Ser	Gly	Asn	Arg	Ser	Ala	Arg	
				245					250					255	

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Pro	Leu	His	Ser	Leu	Ser	Val	Leu	Ala	Phe	Asp	Gln	Glu	Arg	Leu
				260					265					270
Glu	Arg	Lys	Ile	Leu	Ala	Leu	Arg	Gln	Ala	Arg	Arg	Pro	Val	Pro
				275					280					285
Pro	Glu	Val	Ala	Gln	Gln	Tyr	Gln	Asp	Ile	Met	Gln	Arg	Ser	Gln
				290					295					300
Trp	Gln	Arg	Ala	Gln	Leu	Glu	Gln	Gly	Gly	Val	Gly	Ile	Arg	Arg
				305					310					315
Glu	Tyr	Ala	Ala	Gln	Leu	Glu	Arg	Gln	Leu	Gln	Phe	Tyr	Thr	Glu
				320					325					330
Ala	Ala	Arg	Arg	Leu	Gly	Asn	Asp	Gly	Ser	Arg	Asp	Ala	Ala	Lys
				335					340					345
Glu	Ala	Leu	Tyr	Arg	Arg	Asn	Leu	Val	Glu	Ser	Glu	Leu	Gln	Arg
				350					355					360
Leu	Arg	Arg												

<210> 6
 <211> 484
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 2799056

<400> 6

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
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Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
				20					25					30
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
				35					40					45
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
				50					55					60
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
				65					70					75
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
				80					85					90
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
				95					100					105
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
				110					115					120
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
				125					130					135
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
				140					145					150
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
				155					160					165
Arg	Ile	Gln	Leu	Leu	His	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu
				170					175					180
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu
				185					190					195
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly
				200					205					210

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Met Tyr Ala Asp	Leu Leu Gln Leu Val	Lys Val Pro Ile Ser	Leu
	215	220	225
Ser Ile Asp Arg	Leu Glu Phe Asp Leu	Leu Tyr Pro Ala Ile	Lys
	230	235	240
Gly Asp Thr Ile	Gln Leu Tyr Leu Gly	Ala Lys Leu Leu Asp	Ser
	245	250	255
Gln Gly Lys Val	Thr Lys Trp Phe Asn	Asn Ser Ala Ala Ser	Leu
	260	265	270
Thr Met Pro Thr	Leu Asp Asn Ile Pro	Phe Ser Leu Ile Val	Ser
	275	280	285
Gln Asp Val Val	Lys Ala Ala Val Ala	Ala Val Leu Ser Pro	Glu
	290	295	300
Glu Phe Met Val	Leu Leu Asp Ser Val	Leu Pro Glu Ser Ala	His
	305	310	315
Arg Leu Lys Ser	Ser Ile Gly Leu Ile	Asn Glu Lys Ala Ala	Asp
	320	325	330
Lys Leu Gly Ser	Thr Gln Ile Val Lys	Ile Leu Thr Gln Asp	Thr
	335	340	345
Pro Glu Phe Phe	Ile Asp Gln Gly His	Ala Lys Val Ala Gln	Leu
	350	355	360
Ile Val Leu Glu	Val Phe Pro Ser Ser	Glu Ala Leu Arg Pro	Leu
	365	370	375
Phe Thr Leu Gly	Ile Glu Ala Ser Ser	Glu Ala Gln Phe Tyr	Thr
	380	385	390
Lys Gly Asp Gln	Leu Ile Leu Asn Leu	Asn Asn Ile Ser Ser	Asp
	395	400	405
Arg Ile Gln Leu	Met Asn Ser Gly Ile	Gly Trp Phe Gln Pro	Asp
	410	415	420
Val Leu Lys Asn	Ile Ile Thr Glu Ile	Ile His Ser Ile Leu	Leu
	425	430	435
Pro Asn Gln Asn	Gly Lys Leu Arg Ser	Gly Val Pro Val Ser	Leu
	440	445	450
Val Lys Ala Leu	Gly Phe Glu Ala Ala	Glu Ser Ser Leu Thr	Lys
	455	460	465
Asp Ala Leu Val	Leu Thr Pro Ala Ser	Leu Trp Lys Pro Ser	Ser
	470	475	480
Pro Val Ser Gln			

<210> 7
 <211> 1638
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 238506

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 cgggagcccc ggggaccacag agaacgcaag gaggatggct cagcggacgg agaccctgtg 180
 cagattgact tcatcgacag ccatgtcccc ggggaggatg aagagcgagg cactgtggag 240
 gagcagcgac caccgaatt aagccctggg gcaggggaca gggagagggc accaagcagc 300
 aggcgggagg agccggcagg ggaggagcgg cggcgcccg acaccttgca gctgtggcag 360

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atgcacaacg gctcgcctaa gtccagtgcc tcccaagcag gggctgcagc ggggcaggga 540
gcccccgccc ctgcccctgc ctcccaagag ccccttccca tagctggacc agcgacagca 600
cctgctccac ggccacttgg ctccattcag agaccaaaca gcttcctctt ccgttcctcc 660
tctcagagtg gctcaggccc ttctccacca gactctgtcc tgagacctcg gcggtacccc 720
caggttccag atgagaagga cttaatgact cagctgcgcc aggtccttga gtcccggctg 780
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cccccccaa cagctgctat gggggggcta aattatctct atttttaga gaggatctat 1560
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<210> 8
 <211> 1015
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> Incyte Clone No: 414692

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cccgtaccc tcgtcctcg atcgaggacg acttcaacta tggcagcagc gtggcctccg 240
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ttctcttaac tacagtact tcaacagttt ttttatactt tgagtctgta cggacatttg 360
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tgttggaagc tctgactgtg gcagttgttg ttactttcta tgatgtatat attattctgc 540
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agaaggattt cagcaaattt ggagcagggc tgtttgctct tttgtggata ttgtgcctgt 660
caggattctt gaagtttttt ttttatagtg agataatgga gttggtctta gccgtgcag 720
gagcccttct tttctgtgga ttcatcatct atgacacaca ctactgatg cataaactgt 780
cacctgaaga gtacgtatta gctgccatca gcctctactt ggatatcatc aatctattcc 840
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actgaagaac aacaaaaaaa atttaacgag aaaaaaggat taaagtaatt ggaagcagta 960
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<210> 9
 <211> 1481
 <212> DNA
 <213> Homo sapiens

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<220>

<221> misc_feature

<223> Incyte Clone No: 998868

<400> 9

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tgtggcactg cataagcaag ttcttatggg cccatataat ccagacactt gtcttgaggt 180
tggtattcttt gatgtgttgg ggaatgacag gaggagagaa tgggcagccc tgggaaacat 240
gtctaaagag gatgccatgg tggagtgtgt caagctctta aataggtgtt gccatctctt 300
ttcaacatat gttgcgtccc acaaaataga gaaggaagag caagacaaaa aaaggcagga 360
ggaagaggag cgaaggcggc gtgaagagga agaaagagaa cgtctgccaa aggaggaaga 420
gaaacgtagg agagaagaag aggaaaggct tgcaggggcg gcagaggaaa ggagacggat 480
agaagaagaa aggtctcggt tggagcagca aaagcagcag ataatggcag ctttaaactc 540
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ggctgggtct tccttgccca catcatcaaa agtgaatgca actgtaccaa gtaatatgat 780
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ttacaaagtc tggagtctag ggttgggcag aagatgacat ttaatttgga gatttctttt 1440
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<210> 10

<211> 1212

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1296451

<400> 10

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cccgggaccg cgaccccggc cgcccagaga tgaccgcgac cgaagccctc ctgcgcgtcc 180
tcttgctcct gctggctttc ggccacagca cctatggggc tgaatgcttc ccggcctgca 240
acccccaaaa tggattctgc gaggatgaca atgtttgcag gtgccagcct ggctggcagg 300
gtcccccttg tgaccagtgc gtgacctctc ccggtgcct tcacggactc tgtggagaac 360
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aggccggggc ctcccatgcc tctgctgtgt gccccctgg cttctcaggc aatttctgcg 600
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